```
FILE 'REGISTRY' ENTERED AT 09:31:30 ON 21 MAY 2004

=> S REVERSE TRANSCRIPTASE/CN
L1             1 REVERSE TRANSCRIPTASE/CN

=> D

L1   ANSWER 1 OF 1  REGISTRY  COPYRIGHT 2004 ACS on STN
RN   9068-38-6  REGISTRY
CN   Nucleotidyltransferase, deoxyribonucleate, RNA-dependent (9CI)  (CA INDEX
     NAME)
OTHER NAMES:
CN   Reverse transcriptase
CN   Revertase
CN   RNA revertase
CN   RNA-dependent deoxyribonucleate nucleotidyltransferase
CN   RNA-dependent DNA polymerase
CN   RNA-directed DNA polymerase
CN   RNA-instructed DNA polymerase
CN   SuperScript
CN   SuperScript II
CN   ThermoScript
CN   ThermoScript II
MF   Unspecified
CI   MAN
LC   STN Files:   ADISNEWS, AGRICOLA, ANABSTR, BIOBUSINESS, BIOSIS, BIOTECHNO,
       CA, CABA, CAPLUS, CASREACT, CBNB, CEN, CHEMCATS, CHEMLIST, CIN, CSCHEM,
       EMBASE, IFICDB, IFIPAT, IFIUDB, MSDS-OHS, NAPRALERT, PIRA, PROMT,
       TOXCENTER, USPAT2, USPATFULL
     Other Sources:   EINECS**
         (**Enter CHEMLIST File for up-to-date regulatory information)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
           8383 REFERENCES IN FILE CA (1907 TO DATE)
            120 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
           8410 REFERENCES IN FILE CAPLUS (1907 TO DATE)

FILE 'CAPLUS' ENTERED AT 09:32:11 ON 21 MAY 2004

=> S REVERSE TRANSCRIPTASE;S L2 OR L1;S AVIAN MYELOBLASTOSIS VIRUS;S AMV;S AVIAN
MYELOBLAS?
        178382 REVERSE
          7436 REVERSES
        185073 REVERSE
                 (REVERSE OR REVERSES)
         25395 TRANSCRIPTASE
           694 TRANSCRIPTASES
         25527 TRANSCRIPTASE
                 (TRANSCRIPTASE OR TRANSCRIPTASES)
L2       24997 REVERSE TRANSCRIPTASE
                 (REVERSE(W)TRANSCRIPTASE)


          8410 L1
L3       25563 L2 OR L1


         19518 AVIAN
           171 AVIANS
         19612 AVIAN
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                (AVIAN OR AVIANS)
          1620 MYELOBLASTOSIS
        299751 VIRUS
         64365 VIRUSES
        310646 VIRUS
                (VIRUS OR VIRUSES)
L4        1379 AVIAN MYELOBLASTOSIS VIRUS
                (AVIAN(W)MYELOBLASTOSIS(W)VIRUS)


          1057 AMV
             3 AMVS
L5        1058 AMV
                (AMV OR AMVS)


         19518 AVIAN
           171 AVIANS
         19612 AVIAN
                (AVIAN OR AVIANS)
          3588 MYELOBLAS?
L6        1548 AVIAN MYELOBLAS?
                (AVIAN(W)MYELOBLAS?)

=> S L4,L6
L7        1548 (L4 OR L6)

=> S L7 AND L3
L8         801 L7 AND L3

=> S L8 AND L5
L9         199 L8 AND L5

=> S CLON?;S PROKARY? OR PROCARY?;S INDUC?
L10     315376 CLON?


         17393 PROKARY?
           496 PROCARY?
L11      17775 PROKARY? OR PROCARY?


L12    1845162 INDUC?

=> S L8 AND L11
L13          12 L8 AND L11

=> S L8 AND L12
L14          60 L8 AND L12

=> S L14 NOT L12
L15           0 L14 NOT L12

=> S L14 NOT L13
L16          58 L14 NOT L13

=> D L13 1-12 CBIB ABS;D L16 1-58 TI

L13  ANSWER 1 OF 12  CAPLUS  COPYRIGHT 2004 ACS on STN
2002:237920   Document No. 136:258316  Expression vectors for synthesizing
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heterodimeric AMV-RT in Escherichia coli. Sobek, Harald; Mueller, Rainer; Schmidt, Manfred; Frey, Bruno; Suppmann, Bernhard; Schmuck, Rainer; Thalhofer, Johann-Peter; Pallua, Peter; Pajatsch, Markus (Roche Diagnostics Gmbh, Germany; F. Hoffmann-La Roche Ag). Eur. Pat. Appl. EP 1191102 A2 20020327, 28 pp. DESIGNATED STATES: R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO. (English). CODEN: EPXXDW. APPLICATION: EP 2001-121754 20010919. PRIORITY: DE 2000-10046960 20000922.

AB The heterologous expression of the **reverse transcriptase** (α and β subunits) from the **Avian Myeloblastosis Virus** (AMV-RT) in **prokaryotic** cell. In particular Escherichia coli (E. coli) is the host in the present invention. The α- and β-chains of the AMV-RT may be cloned on sep. plasmids or on the same plasmid. Furthermore, the α- and β-chains of AMV-RT may be fused with a peptide sequence composed of 2-10 arginine or 2-10 histidine residues. The DNA sequences encoding the α- and β-chains of AMV-RT which are linked to the DNA sequences encoding the said peptides are capable of reversible binding. Expression of AMV-RT gene may be increased by helper gene co-expression of trpT gene (encodes tryptophan tRNA). Furthermore, chaperone genes GroEL and GroES may be cloned onto said plasmid expressing the α- and β-chains of AMV-RT, and genes for DnaK, DnaJ, GrpE and ClpB may be cloned onto a helper plasmid for improved expression. Expression occurs at growth temperature of 10-25° C and at reduced inducer concentration The said plasmid may be used to generate cDNA by RT-PCR. The invention also includes certain measures to simplify the purification of the active heterodimeric AMV-RT including metal chelators or cation exchangers in affinity chromatog. Specifically, the peptide sequences fused to AMV-RT are capable of reversibly binding resins of the affinity chromatog. apparatus

L13 ANSWER 2 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN

2002:107534 Document No. 136:162282 Gene silencing using mRNA-cDNA hybrids, methods, compositions, and therapeutic uses thereof. Lin, Shi-Lung; Chuong, Cheng-Ming; Widelitz, Randall B. (University of Southern California, USA). PCT Int. Appl. WO 2002010374 A2 20020207, 53 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2001-US24412 20010802. PRIORITY: US 2000-PV222479 20000802.

AB The present invention provides novel compns. and methods for suppressing the expression of a targeted gene using mRNA-cDNA duplexes. The invention further provides novel methods and compns. for generating amplified mRNA-cDNA hybrids, whose quantity is high enough to be used for the invention's gene silencing transfection. This improved RNA-polymerase chain reaction method uses thermocycling steps of promoter-linked double-stranded cDNA or RNA synthesis, in vitro transcription and then reverse transcription to amplify the amount of mRNA-cDNA hybrids up to two thousand folds within one round of the above procedure. The methods and compns. are claimed for use in transfecting cells, organisms and animals, including humans, and for targeting nucleic acids such as pathogenic nucleic acids, viral genes, mutated genes, and oncogenes. One example of the invention is injection of chicken embryos near the liver primordia with β-catenin mRNA-cDNA or cDNA-aRNA to knock out β-catenin expression in the skin and liver. Another example is transfection of androgen-induced LNCaP cells with gene bcl-2 synthetic RNA-DNA hybrids. The methods of the invention are potentially based on an RNA-directed RNA

polymerase-dependent gene silencing phenomenon called DNA-RNA interference, which is thought to be similar to post-transcriptional gene silencing (PTGS) and RNA interference (RNAi).

L13 ANSWER 3 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN
1996:259799 Document No. 124:281101 Use of RNA polymerase to improve nucleic acid amplification. Sooknanan, Roy (Cangene Corporation, Can.). PCT Int. Appl. WO 9602668 A1 19960201, 43 pp. DESIGNATED STATES: W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TT; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 1995-CA423 19950713. PRIORITY: US 1994-275250 19940715.

AB A eukaryotic or **prokaryotic** DNA-directed RNA polymerase of a class that synthesizes cellular RNA, can be used in a process for the amplification of a specific nucleic acid sequence or of its complement. This is a new process for amplifying a specific nucleic acid sequence. The process includes one or more reactions which may take place in a single reaction vessel. In one instance, in a first reaction, the process includes providing a first RNA polymerase which uses a DNA first template to synthesize an RNA first template, and, in a second reaction, providing the RNA first template and a number of other reagents such that the reagents use the RNA first template to synthesize a DNA second template and an RNA second template. Therefore a cycle ensues in which the reagents use the RNA second template to synthesize a DNA third template and multiple copies of the RNA second template. The RNA second template is the specific nucleic acid sequence or its complement. This invention includes a kit containing the reagents of this invention.

L13 ANSWER 4 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN
1995:953784 Document No. 124:254284 High-affinity interaction of human immunodeficiency virus type-1 **reverse transcriptase** with partially complementary primers. Zakharova, Ol'ga D.; Tarrago-Litvak, Laura; Maksakova, Galija; Andreola, Marie-Line; Dufour, Emmanuelle; Litvak, Simon; Nevinsky, Georgy A. (Novosibirsk Inst. Bioorganic Chem., Russia). European Journal of Biochemistry, 233(3), 856-63 (English) 1995. CODEN: EJBCAI. ISSN: 0014-2956. Publisher: Springer.

AB The comparison of Km and Vmax values for various primers in the reaction of polymerization catalyzed by the human immunodeficiency virus type-1 (HIV-1) **reverse transcriptase** was carried out. The primers were: (a) complementary to the template, (b) partially complementary with mismatched nucleotides at different positions from the 3' end or (c) non-complementary. Non-complementary primers were not elongated by HIV-1 **reverse transcriptase**. However, if they contained only one residue complementary to the template or an abasic unit at the 3' end, they could serve as primers. The most effective discrimination between matched and mismatched primers, due to a decrease in the affinity and Vmax, was found in the case of oligonucleotides containing non-complementary bases at the second or third position from the 3' end of the primer. The efficiency of discrimination by HIV-1 **reverse transcriptase** between matched and mismatched base-paired primers was about 1-1.5 orders of magnitude lower than that of **procaryotic** , eucaryotic and archaebacterial DNA polymerases and **avian myeloblastosis virus reverse transcriptase**. Oligonucleotides such as (dT)4(dCdG)k(dT)4 showed higher affinity for the enzyme than (dT)4 or (dT)8 primers. Thus, HIV-1 **reverse transcriptase**, in contrast to **procaryotic**, eucaryotic and archaebacterial DNA polymerases, forms addnl. contacts with the 5'-end region of the non-complementary primer. In addition, using tRNA3Lys, the natural primer of HIV-

1, the p66 subunit of **reverse transcriptase** can be crosslinked, in the presence of a Pt derivative, to the 5' end of tRNA. Thus, besides the normal binding site for the 3' end of tRNA, which is crucial for the initiation of cDNA synthesis, the 5' end of the tRNA also interacts with a specific site on the enzyme.

L13 ANSWER 5 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN

1990:135033 Document No. 112:135033 Conformationally restricted nucleoside 5'-triphosphates as termination substrates for DNA polymerases. Chidzhavadze, Z. G.; Bibilashvilli, R. Sh.; Rozovskaya, T. A.; Tarusova, N. B.; Atrazhev, A. M.; Minasyan, Sh. Kh.; Dyatkina, N. B.; Atrazheva, E. D.; Kukhanova, M. K.; et al. (Natl. Cardiol. Res. Cent., Moscow, USSR). Molekulyarnaya Biologiya (Moscow), 23(6), 1732-42 (Russian) 1989. CODEN: MOBIBO. ISSN: 0026-8984.

AB The ability of some nucleoside 5'-triphosphate analogs to terminate DNA synthesis catalyzed by calf thymus DNA polymerase α and terminal deoxynucleotidyltransferase, rat liver DNA polymerase β, Escherichia coli DNA polymerase I (Klenow fragment) and **avian myeloblastosis virus reverse transcriptase**. Lyxoanhydronucleoside 5'-triphosphates terminate DNA synthesis catalyzed by **reverse transcriptase** and terminal deoxynucleotidyltransferase. 2',3'-O-Isopropylidenecytidine 5'-triphosphate inhibits DNA synthesis catalyzed by **reverse transcriptase** and DNA polymerase β and its moiety was incorporated in the place of dTMP residue. Riboanhydroadenosine 5'-triphosphate was an effective termination substrate for all the DNA polymerases studied.

L13 ANSWER 6 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN

1989:71751 Document No. 110:71751 Novel non-templated nucleotide addition reactions catalyzed by **prokaryotic** and eukaryotic DNA polymerases. Clark, James M. (Lab. Mol. Genet., Natl. Inst. Environ. Health Sci., Research Triangle Park, NC, 27709, USA). Nucleic Acids Research, 16(20), 9677-86 (English) 1988. CODEN: NARHAD. ISSN: 0305-1048.

AB DNA polymerases catalyze the addition of deoxyribonucleotides onto DNA primers in a template-directed manner. The requirement for template instruction distinguishes these enzymes from other nucleotidyltransferases, such as terminal deoxynucleotidyltransferase, that do not utilize a template. An oligonucleotide substrate was used to characterize a novel, nontemplated nucleotide addition reaction carried out by DNA polymerases from a variety of **prokaryotic** and eukaryotic sources. The products of the reaction, in which a deoxyribonucleotide was added to the 3' hydroxyl terminus of a blunt-ended DNA substrate, were analyzed by electrophoresis on high resolution, denaturing polyacrylamide gels. DNA polymerase from Thermus aquaticus, polymerase α from chick embryo, rat polymerase β, **reverse transcriptase** from **avian myeloblastosis virus**, and DNA polymerase I from Saccharomyces cerevisiae all carried out the blunt-end addition reaction. The reaction required a duplex DNA substrate but did not require coding information from the template strand. Apparently, template instruction is not an absolute requirement for the catalysis of nucleotidyl transfer reactions by DNA polymerases.

L13 ANSWER 7 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN

1983:175434 Document No. 98:175434 Rose Bengal mediated inhibition of DNA polymerases. 2. Mechanism of inhibition of **avian myeloblastosis virus reverse transcriptase** under photooxidative conditions. Srivastava, Shiv K.; Modak, Mukund J. (Meml. Sloan-Kettering Cancer Cent., New York, NY,

10021, USA). Biochemistry, 22(9), 2283-8 (English) 1983. CODEN: BICHAW. ISSN: 0006-2960.

AB DNA polymerases from **prokaryotic**, eukaryotic, and oncornaviral sources are irreversibly inactivated upon exposure to Rose Bengal in the presence of light (photooxidn. conditions). Inactivation of these enzymes under dark (nonoxidative) conditions is totally reversible. The primary effect of photooxidn. on the enzyme-Rose Bengal complex was the loss of template-primer binding ability within 5 min of exposure to light. The presence of template-primer, but not the substrate deoxynucleotides, consistently provided partial protection against Rose Bengal-mediated photooxidative inactivation. Preformed enzyme-template-primer complexes were not dissociated by Rose Bengal under these conditions. However, prolonged exposure (25-30 min) of this complex to light in the presence of Rose Bengal led to complete inactivation of catalytic activity without affecting the ability of enzyme to bind to template-primer. Thus, oxidative inactivation of **avian myeloblastosis virus reverse transcriptase** in the presence of Rose Bengal involves a domain within the enzyme that contains the template-primer binding site as well as an addnl. site which is required for the expression of both the polymerization and nuclease activities of the **reverse transcriptase**.

L13 ANSWER 8 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN

1983:13096 Document No. 98:13096 Effect of acetylated and deacetylated 2-aminofluorene adducts on in vitro DNA synthesis. Moore, Peter D.; Rabkin, Samuel D.; Osborn, Ann L.; King, Charles M.; Strauss, Bernard S. (Dep. Microbiol., Univ. Chicago, Chicago, IL, 60637, USA). Proceedings of the National Academy of Sciences of the United States of America, 79(23), 7166-70 (English) 1982. CODEN: PNASA6. ISSN: 0027-8424.

AB Primed .vphi.X174 DNA templates containing either acetylated or deacetylated aminofluorene adducts at the C-8 position of guanine were constructed. T4 DNA polymerase terminates synthesis 1 nucleotide before the acetylated adducts but incorporates an addnl. nucleotide opposite the deacetylated guanylaminofluorene. These observations can be explained by the known preferred conformations of the acetylated and deacetylated guanosinylaminofluorene nucleosides, the former favoring the syn conformation (so that in DNA the guanine is displaced from the helix by the fluorene ring) and the latter preferring the anti conformation (which allows normal base pairing of the guanine with cytosine). A similar differentiation between the 2 adducts was found with Escherichia coli DNA polymerase I. In contrast, **avian myeloblastosis virus** (AMV) **reverse transcriptase**, which terminated with a nucleotide inserted opposite the acetylated adducts, was less able to do so at the deacetylated adducts. The nucleoside incorporated by AMV **reverse transcriptase** opposite the acetylated adduct was exclusively cytidine, which suggests regular base pairing with the reacted guanosine nucleoside in the anti conformation; however, synthesis was completely blocked and unable to continue beyond this point. The differences between the termination patterns of the **prokaryotic** enzymes and of AMV **reverse transcriptase** indicates that specific properties of a replicating polymerase can influence the conformation of a reacted nucleoside in the DNA, thus altering its recognition and possibly its mutagenic activity.

L13 ANSWER 9 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN

1982:506126 Document No. 97:106126 Rose Bengal mediated inhibition of DNA polymerases: mechanism of inhibition of **avian myeloblastosis virus reverse transcriptase** under nonoxidative conditions. Srivastava, Shiv K.; Modak, Mukund J. (Mem. Sloan-Kettering Cancer Cent., New York, NY, 10021, USA). Biochemistry, 21(19), 4633-9 (English) 1982. CODEN: BICHAW. ISSN: 0006-2960.

AB DNA polymerases from eukaryotic, **prokaryotic**, and retroviral sources exhibit strong sensitivity to Rose Bengal (I) dye under dark (nonoxidative) conditions. The mechanism of inhibition by I was investigated by using **avian myeloblastosis virus reverse transcriptase** (II) as a test enzyme. I inhibited both polymerization and II-associated RNase H activity. The inhibition by I was completely reversible, the degree of inhibition being dependent on the final concentration of I in the reaction mixture Kinetic anal. indicated that the inhibition was competitive with respect to the substrate, deoxynucleoside triphosphate, and noncompetitive with respect to the template-primer. The protection against I inhibition was afforded strictly by deoxynucleoside triphosphate that was complementary to template nucleotide. The addition of I to an ongoing reaction consistently inhibited DNA synthesis after a short time lag. Subsequently, studies on the kinetics of polymerization carried out by varying template to primer ratio and incubation temperature indicated that the primary action of I on the ongoing reaction was the prevention of reinitiation, whereas elongation of chains that were already initiated was unaffected. The effect of I on the template-binding function of II, using a Millipore filter binding assay procedure, provided further insight into its mechanism of inhibition, for pretreatment of II with I completely abolished the ability of II to bind to the template-primer, whereas the stability of the preformed enzyme-template complex was unaffected by I addition Preliminary spectrophotofluorometric anal. of I-II complexes indicated that the major site of I reactivity resides in a hydrophobic domain of II, implicating this region as being responsible for stabilizing the binding of enzyme to template.

L13 ANSWER 10 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN
1981:116189 Document No. 94:116189 Sites of termination of in vitro DNA synthesis on ultraviolet- and N-acetylaminofluorene-treated .vphi.X174 templates by **prokaryotic** and eukaryotic DNA polymerases. Moore, Peter D.; Bose, Kallol K.; Rabkin, Samuel D.; Strauss, Bernard S. (Dep. Microbiol., Univ. Chicago, Chicago, IL, 60637, USA). Proceedings of the National Academy of Sciences of the United States of America, 78(1), 110-14 (English) 1981. CODEN: PNASA6. ISSN: 0027-8424.

AB In vitro DNA synthesis on a ϕX174 template primed with a restriction fragment and catalyzed by the Escherichia coli DNA polymerase I large (Klenow) fragment (pol I) terminated at the nucleotide preceding a site altered by UV irradiation or treatment with N-acetylaminofluorene. Termination on UV-irradiated templates was similar when synthesis was catalyzed by E. coli DNA polymerase III holoenzyme (pol III), phage T4 DNA polymerase, a polymerase α from human lymphoma cells, or **avian myeloblastosis virus reverse transcriptase**. Activity of 3'→5' exonuclease was not detected in the **reverse transcriptase** and DNA polymerase α prepns. On N-acetylaminofluorene templates, pol I, pol III, and T4 polymerase reactions terminated immediately preceding the lesion, whereas **reverse transcriptase**-catalyzed reactions and (at some positions in the sequence) polymerase α-catalyzed reactions terminated at the site of the lesion. Substitution of Mn2+ for Mg2+ changed the pattern of pol I-catalyzed termination sites. Termination is apparently a complicated process that does not depend exclusively on the 3'→5' exonuclease activity associated with many polymerases.

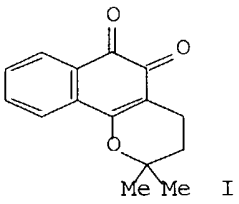
L13 ANSWER 11 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN
1978:611033 Document No. 89:211033 **Reverse transcriptase** -associated RNase H activity. II. Inhibition by natural and synthetic RNA. Marcus, Stuart L.; Smith, Steven W.; Modak, Mukund J. (Mem. Sloan-Kettering Cancer Cent., New York, NY, USA). Journal of Virology, 27(3), 576-81 (English) 1978. CODEN: JOVIAM. ISSN: 0022-538X.

AB The RNase H activity associated with purified **avian myeloblastosis virus** and Rauscher murine leukemia virus DNA polymerases is inhibited by homopolymeric RNA mols., although the efficiency of inhibition by each homopolymer appears enzyme specific. Formation of duplex RNA mols. abolished the inhibitory activity. In contrast to these results, DNA polymerase-independent RNase H activities, such as the RNase H-II from Rauscher murine leukemia virus and calf thymus RNase H, were unaffected by the addition of exogenous RNA mols. to reaction mixts. These results support the concept that the catalytic site of DNA polymerase-associated RNase H activity may be that which is also involved in template binding. Naturally occurring RNA mols. of oncornaviral, **prokaryotic**, or eukaryotic origin also proved to be efficient inhibitors of **avian myeloblastosis virus** DNA polymerase-associated RNase H activity. In contrast to this result, naturally occurring RNA mols., at concns. which inhibited the **avian myeloblastosis virus** enzyme, did not inhibit Rauscher murine leukemia virus DNA polymerase-catalyzed RNase H activity.

L13 ANSWER 12 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN

1978:165933 Document No. 88:165933 β Lapachone, an inhibitor of oncornavirus **reverse transcriptase** and eukaryotic DNA polymerase-α. Inhibitory effect, thiol dependency and specificity. Schuerch, Alfred R.; Wehrli, Walter (Pharm. Div., Ciba-Geigy Ltd., Basel, Switz.). European Journal of Biochemistry, 84(1), 197-205 (English) 1978. CODEN: EJBCAI. ISSN: 0014-2956.

GI



I

AB β-Lapachone is a potent inhibitor of **reverse transcriptase** activity from both **avian myeloblastosis virus** and Rauscher murine leukemia virus. In addition, it affects eukaryotic DNA-dependent DNA polymerase-α activity; 50% inhibition is reached in 60-min incubation time by .apprx.8 μM β-lapachone. The inhibitory effect of the drug is only observed in the presence of dithiothreitol. The primary site of action of β-lapachone appears to be the enzyme protein, as is also borne out by the specificity of its action. Eukaryotic DNA-dependent DNA polymerase-β, **prokaryotic** DNA-dependent DNA polymerase I, several other nucleic acid polymerases, and some completely unrelated enzymes are not affected. **Reverse transcriptase** and DNA-dependent DNA polymerase-α may be in some way related in possessing similarly exposed SH structures in their active sites.

=> D L16 54, 56-58 CBIB ABS

L16 ANSWER 54 OF 58 CAPLUS COPYRIGHT 2004 ACS on STN

1975:108544 Document No. 82:108544 RNA-dependent DNA polymerase (**reverse transcriptase**) from the virus of avian erythroblastosis. Karamucheva, L.; Burny, Arsene; Huez, G.; Marbaix,

Gerard (Bulg.). Izvestiya na Instituta po Obshta i Sravnitelna Patologiya (Bulgarska Akademiya na Naukite), 16, 25-36 (Bulgarian) 1974. CODEN: IIOSAW. ISSN: 0324-0339.

AB Highly active **reverse transcriptase** was found in the virion of erythroblastosis virus. Hybridization between DNA-3H synthesized on erythroblastosis virus as a template and RNA from polysomes of erythroblasts from birds with erythroblastosis revealed virus RNA in these cells. Cross-hybridization between RNA from polysomes of erythroblasts from infected birds and DNA synthesized on **avian myeloblastosis virus** as a template, and vice versa, confirmed virus RNA in erythroblasts and myeloblasts from the peripheral blood of birds affected with leukosis. A common nucleotide sequence of RNA from erythroblastosis and myeloblastosis viruses was found, and this **induced** different forms of avian leukosis. Virus RNA was noted in normal erythroblasts of birds treated with phenylhydrazine, which revealed virus carriage.

L16 ANSWER 56 OF 58 CAPLUS COPYRIGHT 2004 ACS on STN

1974:473862 Document No. 81:73862 RNA-dependent DNA polymerase (**reverse transcriptase**) from **avian myeloblastosis virus**, a zinc metalloenzyme. Auld, D. S.; Kawaguchi, H.; Livingston, D. M.; Vallee, B. L. (Dep. Biol. Chem., Peter Bent Brigham Hosp., Boston, MA, USA). Proceedings of the National Academy of Sciences of the United States of America, 71(5), 2091-5 (English) 1974. CODEN: PNASA6. ISSN: 0027-8424.

AB RNA tumor viruses contain a characteristic RNA-dependent DNA polymerase (**reverse transcriptase**) [**9068-38-6**] which has been thought to be related to the **induction** of leukemia by this virus. A disturbance in a Zn [7440-66-6]-dependent enzyme system was first postulated to account for the demonstrated differences in Zn metabolism of normal and leukemic leukocytes. In order to investigate the relation between Zn and the initiation of leukemia in chickens by **avian myeloblastosis virus**, the metalloenzyme nature of its **reverse transcriptase** was examined The present data show that this protein is a Zn metalloenzyme demonstrating the postulated relation between Zn and a leukemic process. Paucity of purified enzyme generated the design of a novel system of anal. incorporating microwave- **induced** emission spectrometry combined with gel exclusion chromatog. It provides precision, reproducibility, and remarkable limits of detection on μl samples containing 10-12 to 10-14 g-atoms of metal, and is thus, orders of magnitude more sensitive than other methods. The chromatog. fraction with highest enzymic activity contains 1.8 + 10-11 g-atoms of Zn/1.6 μg of protein, corresponding to either 1.8 or 2.0 g-atoms of Zn/mole of enzyme for a mol. weight previously determined either as 1.6 or 1.8 + 105. Cu, Fe, and Mn are absent, i.e., at or below the limits of detection, 10-13 to 10-14 g-atoms. Agents known to chelate Zn inhibit the enzyme, while their nonchelating isomers do not. The data underline the participation of Zn in nucleic acid metabolism and bear importantly upon the lesions that accompany leukemia and Zn deficiency.

L16 ANSWER 57 OF 58 CAPLUS COPYRIGHT 2004 ACS on STN

1974:459958 Document No. 81:59958 **Reverse transcriptase** from **avian myeloblastosis virus**. Zinc metalloenzyme. Auld, D. S.; Kawaguchi, H.; Livingstion, D. M.; Vallee, B. L. (Harvard Med. Sch., Peter Bent Brigham Hosp., Boston, MA, USA). Biochemical and Biophysical Research Communications, 57(4), 967-72 (English) 1974. CODEN: BBRCA9. ISSN: 0006-291X.

AB Previous postulates of a relation between a Zn enzyme and the leukemic process have led to the identification of the **reverse transcriptase** of **avian myeloblastosis virus** as a Zn metalloenzyme. Microwave-**induced** emission spectrometry provides a microanalytical system capable of measuring precisely

10-11-1014 g atoms of metal in μg amts. of enzyme, orders of magnitude more sensitive than other, conventional methods. The chromatog. fraction with highest enzymic activity contained 1.5 x 10-11 g atoms of Zn/1.4 μg of protein, corresponding to 1.7-1.9 g atoms of Zn/mole of enzyme for a mol. weight previously determined either as 1.6 or 1.8 x 105. The Zn/activity ratio was constant in the active fractions. Cu, Fe, and Mn were absent, i.e., at or below their limits of detection, 10-13-10-14 g atoms. Agents known to chelate Zn inhibited the enzyme while their nonchelating isomers did not. The data underline the participation of Zn in nucleic acid metabolism and bear importantly upon the lesions which accompany leukemia and zinc deficiency.

L16 ANSWER 58 OF 58 CAPLUS COPYRIGHT 2004 ACS on STN
1972:537153 Document No. 77:137153 RNA-dependent and DNA-dependent DNA polymerase reactions **induced** by **avian myeloblastosis virus** and feline sarcoma virus.
Fujinaga, Kei; Green, Maurice (Lab. Viral Oncol., Aichi Cancer Cent. Res., Nagoya, Japan). Exp. Leukemogenesis, Pap. Jap. Cancer Ass. Symp. Exp. Leuk. Res. Jap., Meeting Date 1970, 179-89. Editor(s): Yamamoto, Tadashi. Univ. Park Press: Baltimore, Md. (English) 1972. CODEN: 25POAE.
AB A review with 14 refs. DNA polymerase reactions of the virions of **avian myeloblastosis** and feline sarcoma viruses are described. These involve rapid 2-step DNA synthesis reactions in which the initial formation of RNA-DNA hybrid intermediates is followed by the synthesis of duplex DNA mols.

=> S L7 OR L5
L17 2169 L7 OR L5

=> S L17 AND L3
L18 943 L17 AND L3

=> S L18 AND L11
L19 16 L18 AND L11

=> S L18 AND L12
L20 72 L18 AND L12

=> S L19 NOT L13
L21 4 L19 NOT L13

=> D 1-4 CBIB ABS

L21 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2004 ACS on STN
1992:646580 Document No. 117:246580 A comparison of the fidelity of copying 5-methylcytosine and cytosine at a defined DNA template site. Shen, Jiang Cheng; Creighton, Steven; Jones, Peter A.; Goodman, Myron F. (Sch. Med., Univ. South. California, Los Angeles, CA, 90033, USA). Nucleic Acids Research, 20(19), 5119-25 (English) 1992. CODEN: NARHAD. ISSN: 0305-1048.
AB 5-Methylcytosine(mC) has been postulated to be an endogenous mutagen in **prokaryotes** and eukaryotes leading to base substitution hot spots, C→T transitions, resulting from spontaneous deamination of mC to T. The possibility remains, however, that a 2nd mechanism involving mispairing of mC with A might also contribute to base substitution mutagenesis via G→A transitions. Stimulation of the G→A mutational pathway could involve preferential misincorporation of dAMP opposite template mC compared to C. To investigate this possibility a sequence containing mC at a defined template location was synthesized. The fidelity of copying mC vs. C and the efficiency of extending mismatched base pairs at the mC position was compared using 3 DNA

polymerases, **AMV reverse transcriptase**, Drosophila DNA polymerase α (pol α), and mutant Escherichia coli Klenow fragment containing no proofreading exonuclease activity. Significant differences in misinsertion and mismatch extension efficiencies were observed only for the case of **AMV reverse transcriptase** . **AMV reverse transcriptase** was observed to incorporate dAMP 4 to 5-fold more efficiently opposite mC than C. Favored extension of a 5-MeC·A over a C·A mispair was also observed with a difference of about 3-fold. In contrast to **AMV reverse transcriptase**, Klenow fragment showed no significant difference when copying either mC or C sites or when extending mispairs involving mC and C. Incorporation of dAMP opposite either C or mC was barely detectable using pol α, although pol α has been observed to form A·C mismatches in other sequences. While the possibility that dAMP might be incorporated opposite mC in preference to C cannot completely excluded the results suggest that contributions of the G→A pathway to mC mutagenic hot spots are likely to be minor, lending addnl. support to the model invoking deamination of mC.

L21 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2004 ACS on STN

1992:586756 Document No. 117:186756 Oligonucleotides and their derivatives as tools for investigations of protein-nucleic acid interactions in template biocatalysis. Lavrik, O. I. (Inst. Bioorg. Chem., Novosibirsk, 630090, Russia). Nucleic Acids Symposium Series, 24(Synth. Oligonucleotides: Probl. Front. Pract. Appl.), 185-8 (English) 1991. CODEN: NACSD8. ISSN: 0261-3166.

AB A review with 10 refs. On the basis of quant. characteristics (Kd, Km, Gibbs energy values) for the interaction of oligonucleotides with template and primer sites of eucaryotic and **procaryotic** DNA polymerases, a general model of template-primer interaction with these enzymes was suggested. The interactions of **AMV** and HIV **reverse transcriptases** with various 5'-derived oligonucleotides and with human DNA polymerase A and Klenow fragment are compared. The results obtained suggest a method to improve selectively the affinity of an oligonucleotide primer to RNA template with **AMV** and HIV **reverse transcriptases**.

L21 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2004 ACS on STN

1987:612970 Document No. 107:212970 Molecular cloning of genes encoding rat atrium peptides. (Merck and Co., Inc., USA). Jpn. Kokai Tokkyo Koho JP 61161299 A2 19860721 Showa, 15 pp. (Japanese). CODEN: JKXXAF. APPLICATION: JP 1985-32959 19850222. PRIORITY: US 1985-688798 19850104.

GI For diagram(s), see printed CA Issue.

AB DNA sequences II(B=ATT or ATG) encoding atrium sodium excretion factors(ANF) are cloned. and their amino acid sequences I(A = Ile, Met) deduced. Thus, total RNA isolated from rat atrium was made into polyadenylated RNA (polyA+RNA) by oligo dT cellulose. In the 1st chain cDNA preparation, polyA+RNA, human placenta RNase inhibitor, creatine kinase 11-bp primer, 11-bp primer, and avian myoblastoma virus (**AMV**) **reverse transcriptase** were reacted. In the 2nd chain reaction, α-32P-deoxycytidintriphosphate and DNA polymerase I Klenow fragment were reacted with the 1st chain reaction product to give cDNA. The cDNA treated with nuclease was incubated with α-32P-dCTP and terminal deoxynucleotide transcriptase. The cDNA was cloned in pBR322 oligo dG cloning vector. A genomic library of the recombinant plasmid was prepared in Escherichia coli and screened by using pool 1 3'ACCTGXCCXCTCCA5'(X=A, G, C or T) and pool 2 3'ACCTGXCCXCTTCA5' as probes. The cDNA was digested by PST-1 and the PST-1-free cDNA fragment was subcloned in pUC8 at the PST-1 site. Subclone β44 containing a sequence II(B=ATT) encoding ANF was obtained and its amino sequence I(A=Ile) was deduced.

L21 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2004 ACS on STN
1987:418808 Document No. 107:18808 DNA synthesis arrest sites at the right terminus of rat long interspersed repeated (LINE or L1Rn) DNA family members. D'Ambrosio, Ettore; Furano, Anthony V. (Lab. Biochem. Pharmacol., Natl. Inst. Diabetes Dig. Kidney Dis., Bethesda, MD, 20892, USA). Nucleic Acids Research, 15(7), 3155-75 (English) 1987. CODEN: NARHAD. ISSN: 0305-1048.

AB An 150-bp GC-rich (60%) region is at the right end of rat long interspersed repeated DNA (LINE or L1Rn) family members. One of the DNA strands from this region contains several non-palindromic sites that strongly arrest DNA synthesis in vitro by the **prokaryotic** Klenow and T4 DNA polymerases, the eukaryotic α polymerase, and **AMV reverse transcriptase**. The strongest arrest sites are G-rich (.apprx.70%) homopurine stretches of ≥18 residues. Shorter homopurine stretches (≤12 residues) did not arrest DNA synthesis, even if the stretch contains 11/12 G residues. Arrest of the **prokaryotic** polymerases was not affected by their resp. single-stranded binding proteins or polymerase accessory proteins. The region of duplex DNA which contains DNA synthesis arrest sites reacts with bromoacetaldehyde when present in neg.-supercoiled mols. By contrast, homopurine stretches that do not arrest DNA synthesis do not react with bromoacetaldehyde. The presence of bromoacetaldehyde-reactive bases in a G-rich homopurine-containing duplex under torsional stress is thought to be caused by base stacking in the homopurine strand. Therefore, base-stacked regions of the template may arrest DNA synthesis.

=> S L8 AND L10
L22 83 L8 AND L10

=> S L22 NOT (L13,L14,L21)
L23 72 L22 NOT ((L13 OR L14 OR L21))

=> D 1-72 TI
=> D L23 30,47 CBIB ABS

L23 ANSWER 30 OF 72 CAPLUS COPYRIGHT 2004 ACS on STN
1985:517269 Document No. 103:117269 Sites of recombination between the transforming gene of **avian myeloblastosis virus** and its helper virus. Kan, Nancy C.; Baluda, Marcel A.; Papas, Takis S. (Lab. Mol. Oncol., Natl. Cancer Inst., Frederick, MD, 21701, USA). Virology, 145(2), 323-9 (English) 1985. CODEN: VIRLAX. ISSN: 0042-6822.

AB The sites of recombination between the transforming gene of **avian myeloblastosis virus** (AMV) and its natural helper myeloblastosis-associated virus (MAV) were determined In AMV, the cellular sequence substituting for the viral envelope (env) gene gives rise to a different C terminus of the DNA polymerase. The 5'-recombination site coincides with the RNA splice-acceptor site for the production of env mRNA in MAV-infected cells. The 3'-recombination site reveals that the last 11 amino acids including the termination codon are shared by the env protein and AMV transforming protein. The RNA splice-acceptor site for the generation os subgenomic v-myb mRNA is located 84 nucleotides downstream from the 5'-recombination site. The AMV transforming protein consists of helper virus-related sequences at both of its N and C termini, and all but 84 nucleotides of the cell-derived v-myb sequence. The comparison of MAV gp85 amino acid sequence with those of subgroups B, C, and E indicates that the MAV present in **clone** λ10A2-1 belongs to subgroup B. The high degree of homol. among different avian retroviruses of the same subgroup indicates that the amino acid sequence of gp85 is important in determining the conformation of the envelope glycoprotein.

L23 ANSWER 47 OF 72 CAPLUS COPYRIGHT 2004 ACS on STN

1982:486294 Document No. 97:86294 **Cloning** of nucleotide sequences of enzootic bovine leukemia virus (BLV). Liebscher, Dirck Hartmut; Rosenthal, Sinaida; Kettmann, Richard; Burny, Arsene (Akademie der Wissenschaften der DDR, Ger. Dem. Rep.). Ger. (East) DD 153893 Z 19820210, 19 pp. (German). CODEN: GEXXA8. APPLICATION: DD 1980-221834 19800613.

AB DNA sequences complementary to all or part of the RNA genome of bovine leukemia virus (BLV) are inserted in vectors with linkers or by treatment of DNA and vector with appropriate restriction endonucleases, transferred to host cells, and selected after **cloning**. Thus, BLV RNA was recovered as a 70 S complex from sucrose d. gradients, denatured by heat, and reverse transcribed with **avian myeloblastosis virus reverse transcriptase** [**9068-38-6**]. The resulting single strand of BLV cDNA was recovered by sucrose d. gradient centrifugation and RNase [9001-99-4] treatment, and was incubated with DNA polymerase I [9012-90-2] Klenow fragment to give double-stranded BLV cDNA .apprx.2000 base pairs long. The BLV cDNA was tailed with poly(dC) and annealed with endonuclease PstI [81295-32-1]-linearized, poly(dG)-tailed plasmid pBR322. Escherichia coli χ1779 Was transformed with the resulting hybrid plasmids. **Clones** containing plasmids with BLV sequences were identified by in-situ hybridization with BLV [32P]DNA. **Cloned** plasmids with insert lengths of .apprx.600-1400 base pairs were recovered.

	L #	Hits	Search Text	DBs
1	L1	1127	AVIAN ADJ MYELOBLASTOSIS ADJ VIRUS	USPAT ; US-PG PUB
2	L2	24421	REVERSE ADJ TRANSCRIPTASE	USPAT ; US-PG PUB
3	L3	1042	L1 AND L2	USPAT ; US-PG PUB
4	L4	921	L1 SAME L2	USPAT ; US-PG PUB
5	L5	906	L1 NEAR10 L2	USPAT ; US-PG PUB
6	L6	95561	CLON$	USPAT ; US-PG PUB
7	L7	845	L5 AND L6	USPAT ; US-PG PUB
8	L8	37764	PROKARYOT$ OR PROCARYOT$	USPAT ; US-PG PUB
9	L9	497	L4 AND L8	USPAT ; US-PG PUB
10	L10	6	L4 SAME L8	USPAT ; US-PG PUB
11	L11	628556	INDUC$	USPAT ; US-PG PUB
12	L12	712	L11 AND L4	USPAT ; US-PG PUB
13	L13	16	L11 SAME L4	USPAT ; US-PG PUB
14	L14	22	L10 OR L13	USPAT ; US-PG PUB